SEQUENCE LISTING

- (1) GENERAL INFORMATION:
 - (i) APPLICANT: SAMSON, MICHEL PARMENTIER, MARC VASSART, GILBERT LIBERT, FREDERICK
 - (ii) TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
 - (iii) NUMBER OF SEQUENCES: 17
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Knobbe, Martens, Olson & Bear
 - (B) STREET: 620 Newport Center Drive 16th Floor
 - (C) CITY: Newport Beach
 - (D) STATE: CA

4Z

- (E) COUNTRY: U.S.A.
- (F) ZIP: 92660
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/833,752
 - (B) FILING DATE: 9-APR-1997
 - (C) CLASSIFICATION:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Altman, Daniel E
 - (B) REGISTRATION NUMBER: 34,115
 - (C) REFERENCE/DOCKET NUMBER:
- (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 792 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS(B) LOCATION: 240..791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

| GAAT' | TCC | CCC 2 | AACA | GAGC | CA A | GCTC: | rcca: | CTA | AGTG(| GACA | GGGZ | AAGC' | rag (| CAGC | AAACCT | 60 |
|----------------|------|-------------|-------|----------|--------|-------|-------------|-------|-------------|------|----------|----------|---------|------------|-----------|-------------|
| | | | | | | | | | | | | | | | GACATC | 120 |
| | | | | | | | | | | | | | | | GCAACT | 180 |
| | | | | | | | | | | | | | | | ACAAG | 239 |
| ATG | | | | | | | | | | | | | | | | 287 |
| Met . | Asp | Tyr | Gln | Val 5 | Ser | Ser | Pro | Ile | Tyr 10 | Asp | Ile | Asn | Tyr | Tyr 15 | Thr | |
| TCG | GAG | CCC | TGC | CAA | AAA | ATC | AAT | GTG | AAG | CAA | ATC | GCA | GCC | CGC | CTC | 335 |
| Ser | Glu | Pro | _ | Gln | Lys | Ile | Asn | | Lys | Gln | Ile | Ala | Ala | Arg | Leu | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| CTG | | | | | | | | | | | | | | | | 383 |
| Leu | | | Leu | Tyr | Ser | Leu | | Phe | Ile | Phe | Gly | | Val | Gly | Asn | |
| D | | 35 | | | | | 40 | | | | | 45 | | | | |
| ATG | | | | | | | | | | | | | | | | 431 |
| Metil | | Val | lle | Leu | lle | | lle | Asn | Cys | Lys | | Leu | Lys | Ser | Met | |
| | 50 | 3 m.a | | ama. | C TO C | 55 | ama. | ~~~ | 3 m.a | mam | 60 | ama | - | mm a | amm | 450 |
| ACT | | | | | | | | | | | | | | | | 479 |
| Thr 65 | | TIE | тĂт | пеп | 70 | ASII | ьeu | нта | тте | 75 | Asp | ьеu | Pne | Pne | ьеи 80 | |
| CTT | ; | GTC | כככ | ጥጥር | | CCT | $C\Delta C$ | ידעיד | CCT | | CCC | CAG | ТСС | GAC | | 527 |
| Leu | | | | | | | | | | | | | | | | 527 |
| â | | | | 85 | | | ***** | - 1 - | 90 | 1114 | | 0 | | 95 | 1 110 | |
| GGA | AAT | ACA | ATG | TGT | CAA | CTC | TTG | ACA | GGG | CTC | TAT | TTT | ATA | | TTC | 575 |
| Gly | | | | | | | | | | | | | | | | |
| - Am | I | | 100 | _ | | | | 105 | - | | - | | 110 | - | | |
| TTC | TCT | GGA | ATC | TTC | TTC | ATC | ATC | CTC | CTG | ACA | ATC | GAT | AGG | TAC | CTG | 623 |
| Phe | Ser | Gly | Ile | Phe | Phe | Ile | Ile | Leu | Leu | Thr | Ile | Asp | Arg | Tyr | Leu | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| GCT (| | | | | | | | | | | | | | | | 671 |
| Ala | | Val | His | Ala | Val | | Ala | Leu | Lys | Ala | | Thr | Val | Thr | Phe | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| GGG (| | | | | | | | | | | | | | | | 719 |
| Gly V | val | Val | Thr | Ser | | He | Thr | Trp | Val | | Ala | Val | Phe | Ala | | |
| 145 | aa2 | CC3 | 3 M/G | 3.00.0 | 150 | 3.00 | 3 (13 | mam | C 7 7 | 155 | <i>~</i> | aam | - COURT | C B III | 160 | 5 .5 |
| CTC (| | | | | | | | | | | | | | | | 767 |
| Leu l | P.LO | στλ | тте | 11e | rue | inr | arg | ser | GIN 170 | ьys | GIU | GTĀ | ьeu | H1S 175 | Tyr | |
| ACC : | ጥርር | A CC | ጥርጥ | | ւրդ | רכז | ጥአር | 7\ | 1 /0 | | | | | T/2 | | 792 |
| Thr (| | | | | | | | A | | | | | | | | 134 |
| **** | | | 180 | ***** | 2110 | 110 | - Y - | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1477 base pairs
- (B) TYPE: nucleic acid(C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 240..1295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

| GAA' | TTCC | CCC : | AACA | GAGC | CA A | GCTC' | TCCA' | r ct | AGTG | GACA | GGG | AAGC' | TAG | CAGC | AAACCT | 60 |
|-------------|-----------|------------|-----------|--------|-------|-----------|---------|-----------|-------|------|-----------|-------|-----------|------------|--------|-----|
| | | | | | | | | | | | | | | | GACATC | 120 |
| | | | | | | | | | | | | | | | GCAACT | 180 |
| | | | | | | | | | | | | | | | ACAAG | 239 |
| | | | | | | | | | | | | | | TAT | | 287 |
| Met | Asp | Tyr | Gln | Val | Ser | Ser | Pro | Ile | Tyr | Asp | Ile | Asn | Tyr | Tyr | Thr | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| TCG | GAG | CCC | TGC | CAA | AAA | ATC | AAT | GTG | AAG | CAA | ATC | GCA | GCC | CGC | CTC | 335 |
| se n | GLu | Pro | Cys 20 | GIn | ьуs | IIe | Asn | Val 25 | Lys | Gln | Ile | Ala | Ala 30 | Arg | Leu | |
| | | | | | | | | | | | | | | GGC | | 383 |
| Leu | Pro | Pro | Leu | Tyr | Ser | Leu | Val | Phe | Ile | Phe | Gly | Phe | Val | Gly | Asn | |
| 75 | | 35 | | | | | 40 | | | | | 45 | | | | |
| ATG | CTG | GTC | ATC | CTC | ATC | CTG | ATA | AAC | TGC | AAA | AGG | CTG | AAG | AGC | ATG | 431 |
| Met | Leu 50 | Val | Ile | Leu | Ile | Leu 55 | Ile | Asn | Cys | Lys | Arg 60 | Leu | Lys | Ser | Met | |
| ACT | GAC | ATC | TAC | CTG | CTC | AAC | CTG | GCC | ATC | TCT | | CTG | TTT | TTC | CTT | 479 |
| Thr | Asp | Ile | Tyr | Leu | Leu | Asn | Leu | Ala | Ile | Ser | Asp | Leu | Phe | Phe | Leu | |
| 65 | - | | | | 70 | | | | | 75 | _ | | | | 80 | |
| CTT | ACT | GTC | CCC | TTC | TGG | GCT | CAC | TAT | GCT | GCC | GCC | CAG | TGG | GAC | TTT | 527 |
| Leu | Thr | Val | Pro | Phe | Trp | Ala | His | Tyr | Ala | Ala | Ala | Gln | Trp | Asp | Phe | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| GGA | AAT | ACA | ATG | TGT | CAA | CTC | TTG | ACA | GGG | CTC | TAT | TTT | ATA | GGC | TTC | 575 |
| GIY | Asn | Thr | | Cys | Gln | Leu | Leu | | Gly | Leu | Tyr | Phe | Ile | Gly | Phe | |
| mma | m ~m | aa. | 100 | | | | | 105 | | | | | 110 | | | |
| TTC | TCT | GGA | ATC | TTC | TTC | ATC | ATC | CTC | CTG | ACA | ATC | GAT | AGG | TAC | CTG | 623 |
| Pne | Ser | | TTE | Pne | Pne | тте | | Leu | Leu | Thr | Ile | | Arg | Tyr | Leu | |
| CCT | CTC | 115 CTC | CATE | COM | аша | mmm | 120 | | | 999 | 3.00 | 125 | ama | | | c=4 |
| Al = | Wal | Wal | Uic | 77- | GIG | Dho | GCT | TTA | AAA | GCC | AGG | ACG | GTC | ACC | TTT | 671 |
| ALA | 130 | vaı | nis | Ата | vai | 135 | Ата | Leu | гàг | Ala | | Inr | vaı | Thr | Pne | • |
| CCC | | CTC | አርአ | א כיתי | CTC | | 7 (717) | maa | ama | ama | 140 | ama | mmm | aaa | mam | 710 |
| Glv | Val | Val | Thr | Cor | Unl | TIO | Thr | TUU | UTG | GIG | GCT | GIG | LIT | GCG Ala | TCT | 719 |
| 145 | Val | val | TILL | 261 | 150 | 116 | TIII | ıτρ | vai | 155 | Ala | vai | Pne | ALA | | |
| | CCA | GGA | ΔͲϹ | ΔΤΟ | | ACC | አርአ | ጥርጥ | C 7 7 | | מאס | CCT | Cutur | CAT | 160 | 767 |
| Leu | Pro | Glv | Tle | Tle | Phe | Thr | Ara | Ser | CAA | Tare | GAA | Glv | LAII | His | Tur | 707 |
| | | <u>1</u> | | 165 | - 110 | - *** | *** 9 | JCI | 170 | nys | Gru | Ory | шeu | 175 | - Y - | |
| | | | | | | | | | ± / U | | | | | ± , J | | |

| | | | | | | | | | | | CAA | | | | | 815 |
|--------|------|------|------|------|------|------|------|-----|-------|-----|------|------|-------|-------|--------|------|
| Thr | Cys | Ser | | His | Phe | Pro | Tyr | | Gln | Tyr | Gln | Phe | Trp | Lys | Asn | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| | | | | | | | | | | | GTC | | | | | 863 |
| Phe | Gln | | Leu | Lys | Ile | Val | | Leu | Gly | Leu | Val | Leu | Pro | Leu | Leu | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| GTC | ATG | GTC | ATC | TGC | TAC | TCG | GGA | ATC | CTA | AAA | ACT | CTG | CTT | CGG | TGT | 911 |
| Val | | Val | Ile | Cys | Tyr | Ser | Gly | Ile | Leu | Lys | Thr | Leu | Leu | Arg | Cys | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| CGA | AAT | GAG | AAG | AAG | AGG | CAC | AGG | GCT | GTG | AGG | CTT | ATC | TTC | ACC | ATC | 959 |
| Arg | Asn | Glu | Lys | Lys | Arg | His | Arg | Ala | Val | Arg | Leu | Ile | Phe | Thr | Ile | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| ATG | ATT | GTT | TAT | TTT | CTC | TTC | TGG | GCT | CCC | TAC | AAC | ATT | GTC | CTT | CTC | 1007 |
| Met | Ile | Val | Tyr | Phe | Leu | Phe | Trp | Ala | Pro | Tyr | Asn | Ile | Val | Leu | Leu | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| | | | | | | | | | | | AAT | | | | | 1055 |
| Leu | Asn | Thr | Phe | Gln | Glu | Phe | Phe | Gly | Leu | Asn | Asn | Cys | Ser | Ser | Ser | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| AAC | AGG | TTG | GAC | CAA | GCT | ATG | CAG | GTG | ACA | GAG | ACT | CTT | GGG | ATG | ACG | 1103 |
| Asn | Arg | Leu | Asp | Gln | Ala | Met | Gln | Val | Thr | Glu | Thr | Leu | Gly | Met | Thr | |
| 4D | | 275 | | | | | 280 | | | | | 285 | | | | |
| | | | | | | | | | | | GTC | | | | | 1151 |
| His | Cys | Cys | Ile | Asn | Pro | | Ile | Tyr | Ala | Phe | Val | Gly | Glu | Lys | Phe | |
| 771 | 290 | - | | | | 295 | | | | | 300 | | | | | |
| 435 | | | | | | | | | | | ATT | | | | TTC | 1199 |
| 45 480 | Asn | Tyr | Leu | Leu | | Phe | Phe | Gln | Lys | | Ile | Ala | Lys | Arg | Phe | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| 2 | | | | | | | | | | | CCC | | | | | 1247 |
| Cys | Lys | Cys | Cys | | Ile | Phe | Gln | Gln | | Alạ | Pro | Glu | Arg | | Ser | |
| fl | | | | 325 | | | | | 330 | | | | | 335 | | |
| | | | | | | | | | | | ATA | | | | | 1295 |
| Ser | Val | Tyr | | Arg | Ser | Thr | GLY | | Gln | Glu | Ile | Ser | | Gly | Leu | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| | | | | | | | | | | | | | | | TTTCA | 1355 |
| | | | | | | | | | | | | | | | CTGTTA | 1415 |
| | GGGI | CT A | AGAI | TCAT | C CA | TTTA | TTTG | GCA | ATCTO | TTT | AAAG | TAGE | ATT P | AGATO | CCGAAT | 1475 |
| TC | | | | | | | | | | | | | | | | 1477 |

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS

(B) LOCATION: 240..884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

| GAA' | TTCC | CCC 1 | AACA | GAGC | CA A | GCTC' | TCCA: | r ct. | AGTG(| GACA | GGG | AAGC' | TAG | CAGC | AAACCT | 60 |
|--------------|------------|------------|------------|----------|------|------------|------------|------------|-----------|-------|------------|------------|---------------|-----------|--------|------|
| TCC | CTTC | ACT A | ACAA | AACT | rc a | TTGC | rtgg | C CA | AAAA | GAGA | GTT | TTAA | CAA ' | TGTA | GACATC | 120 |
| TAT | GTAG | GCA I | ATTA | AAAA) | CC T | ATTG | ATGT | A TA | AAAC | AGTT | TGC | ATTC: | ATG (| GAGG | GCAACT | 180 |
| AAA' | TACA' | TTC ' | TAGG | ACTT: | ra T | AAAA(| GATC | A CT | TTTT. | TTTA | ATG | CACA | GGG ' | TGGA | ACAAG | 239 |
| | | | | | | | CCA | | | | | | | | | 287 |
| Met 1 | Asp | Tyr | Gln | Val 5 | Ser | Ser | Pro | Ile | Tyr 10 | Asp | Ile | Asn | Tyr | Tyr 15 | Thr | |
| TCG | GAG | CCC | TGC | CAA | AAA | ATC | AAT | GTG | AAG | CAA | ATC | GCA | GCC' | CGC | CTC | 335 |
| Ser | Glu | Pro | Cys 20 | Gln | Lys | Ile | Asn | Val 25 | Lys | Gln | Ile | Ala | Ala 30 | Arg | Leu | |
| CTG | CCT | CCG | CTC | TAC | TCA | CTG | GTG | TTC | ATC | TTT | GGT | TTT | GTG | GGC | AAC | 383 |
| Leu | Pro | Pro 35 | Leu | Tyr | Ser | Leu | Val 40 | Phe | Ile | Phe | Gly | Phe 45 | Val | Gly | Asn | |
| ATG <u>.</u> | CTG | GTC | ATC | CTC | ATC | CTG | ATA | AAC | TGC | AAA | AGG | CTG | AAG | AGC | ATG | 431 |
| | Leu 50 | Val | Ile | Leu | Ile | Leu 55 | Ile | Asn | Cys | Lys | Arg 60 | Leu | Lys | Ser | Met | |
| ACT | GAC | ATC | TAC | CTG | CTC | AAC | CTG | GCC | ATC | TCT | GAC | CTG | TTT | TTC | CTT | 479 |
| Thr | Asp | Ile | Tyr | Leu | Leu | Asn | Leu | Ala | Ile | Ser | Asp | Leu | Phe | Phe | Leu | |
| 65, | Hard . | | | | 70 | | | | | 75 | | | | | 80 | |
| CTŢ: | ACT | GTC | CCC | TTC | TGG | GCT | CAC | TAT | GCT | GCC | GCC | CAG | TGG | GAC | TTT | 527 |
| a. | 7 | | | 85 | | | His | | 90 | | | | _ | 95 | | |
| GGA | AAT | ACA | ATG | TGT | CAA | CTC | TTG | ACA | GGG | CTC | TAT | TTT | ATA | GGC | TTC | 575 |
| Gly | Asn | Thr | Met 100 | Cys | Gln | Leu | Leu | Thr 105 | Gly | Leu | Tyr | Phe | Ile 110 | Gly | Phe | |
| TTĆ | TCT | GGA | ATC | TTC | TTC | ATC | ATC | | CTG | ACA | ATC | GAT | AGG | TAC | CTG | 623 |
| Phe | Ser | Gly 115 | Ile | Phe | Phe | Ile | Ile 120 | Leu | Leu | Thr | Ile | Asp 125 | Arg | Tyr | Leu | |
| GCT* | GTC | GTC | CAT | GCT | GTG | TTT | GCT | TTA | AAA | GCC | AGG | | GTC | ACC | TTT | 671 |
| Ala | Val 130 | Val | His | Ala | Val | Phe 135 | Ala | Leu | Lys | Ala | Arg 140 | Thr | Val | Thr | Phe | |
| GGG | GTG | GTG | ACA | AGT | GTG | ATC | ACT | TGG | GTG | GTG | GCT | GTG | TTT | GCG | TCT | 719 |
| Gly | Val | Val | Thr | Ser | Val | Ile | Thr | Trp | Val | Val | Ala | Val | Phe | Ala | Ser | , 23 |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| CTC | CCA | GGA | ATC | ATC | TTT | ACC | AGA | TCT | CAA | AAA | GAA | GGT | CTT | CAT | TAC | 767 |
| Leu | Pro | Gly | Ile | Ile | Phe | Thr | Arg | Ser | Gln | Lys | Glu | Gly | Leu | His | Tyr | |
| - | | | | 165 | | | | | 170 | | | | | 175 | | |
| ACC | TGC | AGC | TCT | CAT | TTT | CCA | TAC | ATT | AAA | GAT | AGT | CAT | CTT | GGG | GCT | 815 |
| | | | 180 | | | | Tyr | 185 | | | | | 190 | | | |
| GGT | CCT | GCC | GCT | GCT | TGT | CAT | GGT | CAT | CTG | CTA | CTC | GGG | AAT | CCT | AAA | 863 |
| Gly | Pro | Ala | Ala | Ala | Cys | His | Gly | His | Leu | Leu | Leu | Gly | Asn | Pro | Lys | |
| | | 195 | | | | | 200 | | | | | 205 | | | _ | |
| AAC | TCT | GCT | TCG | GTG | TCG | AAA | TGAG | AAGA | AG A | AGGCA | CAGG | G CI | rgtg <i>i</i> | AGGCT | | 914 |
| Asn | Ser 210 | Ala | Ser | Val | Ser | Lys 215 | | | | | | | | | | |
| TATO | TTCA | CC A | TCAT | GATT | G TI | TATT | TTCT | CT1 | CTGG | GCT | CCCI | TACAF | ACA 1 | TGTC | CTTCT | 974 |

| CCTGAACACC | TTCCAGGAAT | TCTTTGGCCT | GAATAATTGC | AGTAGCTCTA | ACAGGTTGGA | 1034 |
|------------|------------|------------|------------|------------|------------|------|
| CCAAGCTATG | CAGGTGACAG | AGACTCTTGG | GATGACGCAC | TGCTGCATCA | ACCCCATCAT | 1094 |
| CTATGCCTTT | GTCGGGGAGA | AGTTCAGAAA | CTACCTCTTA | GTCTTCTTCC | AAAAGCACAT | 1154 |
| TGCCAAACGC | TTCTGCAAAT | GCTGTTCTAT | TTTCCAGCAA | GAGGCTCCCG | AGCGAGCAAG | 1214 |
| CTCAGTTTAC | ACCCGATCCA | CTGGGGAGCA | GGAAATATCT | GTGGGCTTGT | GACACGGACT | 1274 |
| CAAGTGGGCT | GGTGACCCAG | TCAGAGTTGT | GCACATGGCT | TAGTTTTCAT | ACACAGCCTG | 1334 |
| GGCTGGGGGT | GGTTGGGAGG | TCTTTTTTAA | AAGGAAGTTA | CTGTTATAGA | GGGTCTAAGA | 1394 |
| TTCATCCATT | TATTTGGCAT | CTGTTTAAAG | TAGATTAGAT | CCGAATTC | | 1442 |

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 184 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

| 7.55 | | | | | | | | | | | | | | |
|----------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| MetuAsp | Tyr | Gln | Val 5 | Ser | Ser | Pro | Ile | Tyr 10 | Asp | Ile | Asn | Tyr | Tyr 15 | Thr |
| Ser Glu | Pro | Cys 20 | Gln | Lys | Ile | Asn | Val 25 | Lys | Gln | Ile | Ala | Ala 30 | | Leu |
| Leuipro | Pro 35 | Leu | Tyr | Ser | Leu | Val 40 | Phe | Ile | Phe | Gly | Phe 45 | Val | Gly | Asn |
| Met Leu 50 | | Ile | Leu | Ile | Leu 55 | Ile | Asn | Cys | Lys | Arg 60 | Leu | Lys | Ser | Met |
| Thr Asp | Ile | Tyr | Leu | Leu 70 | Asn | Leu | Ala | Ile | Ser 75 | Asp | Leu | Phe | Phe | Leu 80 |
| LeuThr | Val | Pro | Phe 85 | Trp | Ala | His | Tyr | Ala 90 | Ala | Ala | Gln | Trp | Asp 95 | Phe |
| Gly Asn | Thr | Met 100 | Cys | Gln | Leu | Leu | Thr 105 | Gly | Leu | Tyr | Phe | Ile 110 | Gly | Phe |
| Phe Ser | Gly 115 | Ile | Phe | Phe | Ile | Ile 120 | Leu | Leu | Thr | Ile | Asp 125 | Arg | Tyr | Leu |
| Ala Val 130 | Val | His | Ala | Val | Phe 135 | Ala | Leu | Lys | Ala | Arg 140 | Thr | Val | Thr | Phe |
| Gly Val 145 | Val | Thr | Ser | Val 150 | Ile | Thr | Trp | Val | Val 155 | Ala | Val | Phe | Ala | Ser 160 |
| Leu Pro | Gly | Ile | Ile 165 | Phe | Thr | Arg | Ser | Gln 170 | Lys | Glu | Gly | Leu | His 175 | |
| Thr Cys | Ser | Ser 180 | His | Phe | Pro | Tyr | | | | | | | | |
| | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 352 amino acids
 - (B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

| Met 1 | Asp | Tyr | Gln | Val 5 | Ser | Ser | Pro | Ile | Tyr 10 | Asp | Ile | Asn | Tyr | Tyr 15 | Thr |
|----------|-----|-----|-----------|----------|------------|-----|-----|------------|-----------|-----|-----|-----|------------|-----------|-----|
| Ser | Glu | Pro | Cys 20 | Gln | Lys | Ile | Asn | Val 25 | | Gln | Ile | Ala | Ala | Arg | Leu |
| | | 35 | | | Ser | | 40 | | | | | 45 | Val | | |
| | 50 | | | | Ile | 55 | | | | | 60 | Leu | | | |
| 65 | | | | | Leu 70 | | | | | 75 | | | | | 80 |
| | | | | 85 | Trp | | | | 90 | | | | | 95 | Phe |
| 4.11 | | | TOO | | Gln | | | 105 | | | | | 110 | | |
| į. | | TTD | | | Phe | | 120 | | | | | 125 | | | |
| ٩, ۽ | 130 | | | | Val | 135 | | | | | 140 | | | | |
| _++₽; | | | | | Val 150 | | | | | 155 | | | | | 160 |
| 2== | | | | 165 | Phe | | | | 170 | | | | | 175 | |
| 610 0 | | | TRO | | Phe | | | 185 | | | | | 190 | | |
| the same | | 195 | | | Ile | | 200 | | | | | 205 | | | |
| £ | ZTO | | | | Tyr | 215 | | | | | 220 | | | _ | _ |
| 443 | | | | | Arg 230 | | | | | 235 | | | | | 240 |
| | | | | 245 | Leu | | | | 250 | | | | | 255 | |
| | | | 260 | | Glu | | | 265 | | | | | 270 | | |
| | | 4/5 | | | Ala | | 280 | | | | | 285 | | | |
| | 290 | | | | Pro | 295 | | | | | 300 | | | | |
| 303 | | | | | Val 310 | | | | | 315 | | | | | 320 |
| | | | | 325 | Ile | | | | 330 | | | | | 335 | |
| SEL | val | ıyr | 340 | Arg | Ser | Thr | GIY | Glu 345 | Gln | Glu | Ile | Ser | Val 350 | Gly | Leu |

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 215 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr 10 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu 25 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met 55 Tha Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu Lew Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe 85 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe 100 105 110 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu 115 120 125 Ala Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe 130 135 Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser 150 Leg Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr 165 170 Thr Cys Ser Ser His Phe Pro Tyr Ile Lys Asp Ser His Leu Gly Ala 185 Gly Pro Ala Ala Cys His Gly His Leu Leu Gly Asn Pro Lys 200 205 Asn Ser Ala Ser Val Ser Lys 210 215

- (2) INFORMATION FOR SEQ ID NO:7:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: None
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Met Leu Ser Thr Ser Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser
                                     10
Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys
His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu
                             40
Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val
Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr
                     70
Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Ile Ile Thr Leu Pro
                                     90
Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met
                                 105
Cys Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile
                             120
Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His
                         135
                                             140
Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr
                    150
                                         155
Ser Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile
                165
                                     170
Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro
            180
                                 185
Typ Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile
        195
                             200
Lew Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly
                        215
Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg
                    230
                                         235
Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp
                245
                                     250
    Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe
            260
                                 265
                                                     270
Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Ile Gln
                             280
                                                 285
Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile
                        295
                                             300
Tyr Ala Phe Val Gly Glu Lys Phe Arg Arg Tyr Ile Ser Val Phe Phe
                    310
                                         315
Arg Lys His Ile Xaa Xaa Xaa Phe Cys Lys Gln Cys Pro Val Phe Tyr
                325
                                     330
Arg Glu Thr Val Asp Gly Val Thr Ser Thr Asn Thr Pro Ser Thr Gly
            340
                                 345
                                                     350
Glu Gln Glu Val Ser Ala Gly Leu
        355
                             360
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: None
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

| Met 1 | Thr | Thr | Ser | Ile 5 | Asp | Thr | Val | Glu | Thr 10 | Phe | Gly | Thr | Thr | Ser 15 | Tyr |
|-------------|-----------|-----------|------------|----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|------------|
| Tyr | Asp | Asp | Val 20 | Gly | Leu | Leu | Cys | Glu 25 | Lys | Ala | Asp | Thr | Arg 30 | Ala | Leu |
| Met | Ala | Gln 35 | Phe | Val | Pro | Pro | Leu 40 | Tyr | Ser | Leu | Val | Phe 45 | Thr | Val | Gly |
| Leu | Ile 50 | Gly | Asn | Val | Val | Val 55 | Val | Met | Ile | Leu | Ile 60 | Lys | Tyr | Arg | Arg |
| Ile 65 | Arg | Ile | Met | Thr | Asn 70 | Ile | Tyr | Leu | Leu | Asn 75 | Leu | Ala | Ile | Ser | Asp 80 |
| 57 miles | | | Ile | 85 | | | | | 90 | | | _ | | 95 | _ |
| A PAR | | _ | Val 100 | | _ | | _ | 105 | _ | | | | 110 | | |
| [g | | 115 | Gly | | _ | | 120 | | | | | 125 | | | |
| Ile | 130 | | Tyr | | | 135 | | | | | 140 | | | | |
| Arg 145 | | | Thr | | 150 | | | | | 155 | | | _ | | 160 |
| | | | Ala | 165 | | | | | 170 | , | | | | 175 | |
| Leu | | | Glu 180 | | | - | | 185 | | _ | | | 190 | | |
| Tyr | | 195 | Arg | | | | 200 | | _ | | | 205 | | _ | |
| Val | 210 | | Leu | | | 215 | | | _ | - | 220 | | | | |
| 225 | | | Arg | _ | 230 | | | | _ | 235 | _ | | | | 240 |
| | | | Ile | 245 | | | | | 250 | | _ | | | 255 | |
| | | | Leu 260 | | | | _ | 265 | | | | | 270 | | |
| | | 275 | Ser | _ | | | 280 | | | | | 285 | | | |
| | 290 | _ | Ser | | _ | 295 | | | | | 300 | _ | | | |
| 305 | | _ | | | 310 | - | | | | 315 | | | | | Leu 320 |
| | | | Leu | 325 | - | _ | | | 330 | | | | | 335 | |
| | _ | | Ser 340 | Ser | Val | Ser | Pro | Ser 345 | Thr | Ala | Glu | Pro | Glu 350 | Ile | Ser |
| Ile | Val | Phe | | | | | | | | | | | | | |

355

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Glu Thr Pro Asn Thr Thr Glu Asp Tyr Asp Thr Thr Thr Glu Phe Asp Tyr Gly Asp Ala Thr Pro Cys Gln Lys Val Asn Glu Arg Ala Phe 25 GTy Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Val Ile Gly 40 Lêu Val Gly Asn Ile Leu Val Val Leu Val Leu Val Gln Tyr Lys Arg Lieu Lys Asn Met Thr Ser Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Ile Phe Thr Leu Pro Phe Trp Ile Asp Tyr Lys Leu Lys Asp Asp Trp Val Phe Gly Asp Ala Met Cys Lys Ile Ile Ser Gly Phe 105 Tyr Tyr Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr 120 The Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Ile Arg Ala 135 140 Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Ile Ile Trp Ala Ile 150 155 Ala Ile Ile Ala Ser Met Pro Gly Leu Tyr Phe Ser Lys Thr Gln Trp 170 165 Glu Phe Thr His His Thr Cys Ser Leu His Phe Pro His Glu Ser Leu 185 Arg Glu Trp Lys Leu Phe Gln Ala Leu Lys Leu Asn Leu Phe Gly Leu 205 200 Val Leu Pro Leu Leu Val Met Ile Ile Cys Tyr Ile Gly Ile Ile Lys 210 220 215 Ile Leu Leu Arg Arg Pro Asn Glu Lys Lys Ser Lys Ala Val Arg Leu 235 230 Ile Phe Val Ile Met Ile Ile Phe Phe Leu Phe Trp Ile Pro Tyr Asn 250 245 Leu Thr Ile Ile Ser Val Phe Gln Asp Phe Leu Phe Thr His Glu 265 Cys Glu Gln Ser Arg His Leu Asp Leu Ala Val Gln Val Thr Glu Val 280 285 Ile Ala Tyr Thr His Cys Cys Val Asn Glu Val Ile Tyr Ala Phe Val 295

Gly Glu Arg Phe Arg Lys Tyr Ile Arg Gln Leu Glu His Arg Arg Val 305 310 315 320 Ala Val His Leu Val Lys Trp Leu Pro Phe Leu Ser Val Asp Arg Ile 325 330 335 Glu Arg Val Ser Ser Thr Ser Pro Ser Thr Gly Glu His Glu Ile Ser 340 345 350 Ala Gly Phe 355

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: None

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile Tyr Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu 25 Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu 40 Val Glu Val Phe Gly Leu Ile Gly Asn Ser Val Val Val Leu Val Leu the Lys Tyr Lys Arg Ile Arg Ser Met Thr Asp Val Tyr Leu Leu Asn 75 Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly 90 Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Ile Cys Lys Met 105 Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val 120 Met Ile Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Glu 135 140 Xaa Xaa Xaa Ala Arg Thr Ile Ile Tyr Gly Val Ile Thr Ser Leu Ala 150 155 Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Ile Phe Ser 165 170 Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr Ser 185 Leu Asn Ser Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn Ile 200 Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser Met 215 220 Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala 230 235 Val Lys Met Ile Phe Ala Val Val Leu Phe Leu Gly Phe Trp Thr

250 245 Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val 265 Ile Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala 275 280 285 Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr 295 300 Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Ile Gln Leu Phe Lys 310 315 Xaa Xaa Xaa Gly Leu Phe Val Ile Cys Gln Tyr Cys Gly Leu Leu Gln 325 330 Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr Met 345 Asp His Asp Leu His Asp Ala Leu 355

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn 5 10 15

Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu 25 30

Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys 35 40 45

Arg Asn Glu Lys Lys Arg

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 147 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTCCATACA GTCAGTATCA ATTCTGGAAG AATTTCCAGA CATTAAAGAT AGTCATCTTG
GGGCTGGTCC TGCCGCTGCT TGTCATGGTC ATCTGCTACT CGGGAATCCT AAAAACTCTG
120
CTTCGGTGTC GAAATGAGAA GAAGAGG

| | (2) INFORMATION FOR SEQ ID NO:13: | |
|--|---|----|
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13: | |
| 1 | Pro Tyr Ile Lys Asp Ser His Leu Gly Ala Gly Pro Ala Ala Ala 5 10 15 | |
| Cys | His Gly His Leu Leu Gly Asn Pro Lys Asn Ser Ala Ser Val 20 25 30 Lys | |
| | | |
| | (2) INFORMATION FOR SEQ ID NO:14: | |
| The first state true from the same and | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 27 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear | |
| TEG | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14: | 27 |
| · · · · · · · · · · · · · · · · · · · | (2) INFORMATION FOR SEQ ID NO:15: | |
| Ca Salari And America | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 27 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15: | |
| CTG. | ATCTAGA GCCATGTGCA CAACTCT | 27 |
| | (2) INFORMATION FOR SEQ ID NO:16: | |
| | (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear | |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

| CCTGGCTGTC GTCCATGCTG | 20 |
|--|----|
| (2) INFORMATION FOR SEQ ID NO:17: | |
| (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 27 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17: | |
| CTGATCTAGA GCCATGTGCA CAACTCT | 27 |
| | |